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<110> Krueger, Bruce K.
      Kingsbury, Tami J.
      Bambrick, Linda L.
      Dorsey, Susan G.

<120> Novel Treatment of Neurodegenerative Diseases by Altering
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65                  70                  75                  80
Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
                85                  90                  95
Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala Tyr Lys Ala Phe Leu
            100                 105                 110
Lys Asn Ser Asn Leu Arg His Ile Asn Phe Thr Arg Asn Lys Leu Thr
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Ser Leu Ser Arg Arg His Phe Arg His Leu Asp Leu Ser Asp Leu Ile
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Leu Asn Glu Ser Ser Lys Asn Met Pro Leu Ala Asn Leu Gln Ile Pro
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Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
            260                     265                     270
Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
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Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
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305                     310                     315                     320
Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His Val
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Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
            340                     345                     350
His Met Asn Asn Gly Asp Tyr Thr Leu Met Ala Lys Asn Glu Tyr Gly
        355                     360                     365
Lys Asp Glu Arg Gln Ile Ser Ala His Phe Met Gly Arg Pro Gly Val
    370                     375                     380
Asp Tyr Glu Thr Asn Pro Asn Tyr Pro Glu Val Leu Tyr Glu Asp Trp
385                     390                     395                     400
Thr Thr Pro Thr Asp Ile Gly Asp Thr Thr Asn Lys Ser Asn Glu Ile
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Pro Ser Thr Asp Val Ala Asp Gln Ser Asn Arg Glu His Leu Ser Val
            420                     425                     430
Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val
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Met Leu Leu Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys
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<309> 2002-02-07

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gacgatggga acctcttccc cctcctggaa gggcaggatt cagggaacag caatgggaac 360
gccagtatca acatcacgga catctcaagg aatatcactt ccatacacat agagaactgg 420
cgcagtcttc acacgctcaa cgccgtggac atggagctct acaccggact tcaaaagctg 480
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<309> 2002-02-07

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Pro Ala Asn Cys Val Cys Ser Lys Thr Glu Ile Asn Cys Arg Arg Pro
            35                  40                  45
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Thr Ser Ile His Ile Glu Asn Trp Arg Ser Leu His Thr Leu Asn Ala
            85                  90                  95
Val Asp Met Glu Leu Tyr Thr Gly Leu Gln Lys Leu Thr Ile Lys Asn
        100                 105                 110
Ser Gly Leu Arg Ser Ile Gln Pro Arg Ala Phe Ala Lys Asn Pro His
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Leu Arg Tyr Ile Asn Leu Ser Ser Asn Arg Leu Thr Thr Leu Ser Trp
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145                 150                 155                 160
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                165                 170                 175
Gln Gly Glu Ala Lys Leu Asn Ser Gln Asn Leu Tyr Cys Ile Asn Ala
            180                 185                 190
Asp Gly Ser Gln Leu Pro Leu Phe Arg Met Asn Ile Ser Gln Cys Asp
            195                 200                 205
Leu Pro Glu Ile Ser Val Ser His Val Asn Leu Thr Val Arg Glu Gly
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Asp Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp
225                 230                 235                 240
Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln Thr
                245                 250                 255
Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu Val Asn
            260                 265                 270
Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile Ala Glu Asn
    275                 280                 285
Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr Val Tyr Tyr Pro
    290                 295                 300
Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu Arg Leu Glu His Cys
305                 310                 315                 320
Ile Glu Phe Val Val Arg Gly Asn Pro Pro Pro Thr Leu His Trp Leu
                325                 330                 335
His Asn Gly Gln Pro Leu Arg Glu Ser Lys Ile Ile His Val Glu Tyr
            340                 345                 350
Tyr Gln Glu Gly Glu Ile Ser Glu Gly Cys Leu Leu Phe Asn Lys Pro
            355                 360                 365
Thr His Tyr Asn Asn Gly Asn Tyr Thr Leu Ile Ala Lys Asn Pro Leu
370                 375                 380
Gly Thr Ala Asn Gln Thr Ile Asn Gly His Phe Leu Lys Glu Pro Phe
385                 390                 395                 400
Pro Glu Ser Thr Asp Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr
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Pro Pro Ile Thr Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val
            420                 425                 430
Ser Ile Ala Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val
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Leu Phe Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met
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Lys Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro
465                 470                 475                 480
Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp Ala
            485                 490                 495
Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val Ile Glu
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545                      550                      555                      560
Ser Pro Thr Lys Asp Lys Met Leu Val Ala Val Lys Ala Leu Lys Asp
                565                      570                      575
Pro Thr Leu Ala Ala Arg Lys Asp Phe Gln Arg Glu Ala Glu Leu Leu
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Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Gly
        595                      600                      605
Asp Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
    610                      615                      620
Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Met Ile Leu Val
625                      630                      635                      640
Asp Gly Gln Pro Arg Gln Ala Lys Gly Glu Leu Gly Leu Ser Gln Met
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Leu His Ile Ala Ser Gln Ile Ala Ser Gly Met Val Tyr Leu Ala Ser
            660                      665                      670
Gln His Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly
        675                      680                      685
Ala Asn Leu Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val
    690                      695                      700
Tyr Ser Thr Asp Tyr Tyr Arg Leu Phe Asn Pro Ser Gly Asn Asp Phe
705                      710                      715                      720
Cys Ile Trp Cys Glu Val Gly Gly His Thr Met Leu Pro Ile Arg Trp
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Met Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp
            740                      745                      750
Val Trp Ser Phe Gly Val Ile Leu Trp Glu Ile Phe Thr Tyr Gly Lys
        755                      760                      765
Gln Pro Trp Phe Gln Leu Ser Asn Thr Glu Val Ile Glu Cys Ile Thr
    770                      775                      780
Gln Gly Arg Val Leu Glu Arg Pro Arg Val Cys Pro Lys Glu Val Tyr
785                      790                      795                      800
Asp Val Met Leu Gly Cys Trp Gln Arg Glu Pro Gln Gln Arg Leu Asn
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taatactgac cattaattcc cccatgtctg cctcttctgc cagggtcttt tcaaacata 720
gacaatcatg ggatattaaa cttgaaggac aatagagatc atctagtccc atcaactcac 780
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gagttacctc ctttgacgtc tttgtatgca gtaaagatcc ctcccctaac caattttggt 900
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<309> 2000-11-29

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ttttctgtt ttttttcтт tттgttтттт ataggtttca gagaaattat gttgaatcca 240
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<212> DNA
<213> Mus musculus

<220>
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     for mouse TrkB.T1

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ctatcagtcg cagggttgta ggtggaaatc acagaagtta gcaaaggtta gagaacagaa 300
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<213> Mus musculus

<220>
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<210> 19
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<212> DNA
<213> Homo sapiens

<220>
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cattggtgtt ccccaatcac agctcacagt atatgcaggc ttcatatagt acagcctcca 180
aacaccgccc acatctacca gaaaaccca gataagcagc acttcccggg ataagccaac 240
agcagtccca ggagtccagc ttacatggca gcatcaacca acaagcacca gcccctttt 300
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<213> Homo sapiens

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<220>
<221> misc_feature
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    TrkB.Shc

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ctaggttatg gaagctaagg agtgacgtca agatgttgtc tggccagaat ttgcagataa 180
ccatagaact cttctcctcc atcaggcatg gatttagcct cctttagttc ctgcagtgac 240
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<210> 21
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<212> DNA
<213> Homo sapiens

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<223> Anti-sense RNA complementary to human truncated
    TrkC exon 13B

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ggtcttaaga accaaaattg gttaggggag ggatctttac tgcatacaaa gacgtcaaag 180
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gtcagtatta accccaagt gcaaaaaaca tgggaaagta tttttcttaa gtgcacaatg 420
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catcattgcc attcagagtg tcattcctgg gcctggatgg atgtttcttc tgacttggga 720
gataatcctg acccaagac cctctttctg gcttctaata tcccatcaaa aaaattcagc 780
taattttcaa gaggaaagca atgtgacaag gcggggatga tgaggagatg agaggaggtg 840
gtggtgtttg gttccttaaa atcttccttg ccattgttag ggcataaacc attggaaaaa 900
ccaaagctgt tagctcactg aagacctgaa gactacaact tctataaaga gatatcattg 960
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tccgtgtcgg 1030

<210> 22
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<212> DNA
<213> Homo sapiens

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gcaagtatgt cccaaaaaag gatgattttt ccaccgaaaa taaaaataaa aatgtaaagt 180
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